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Cohen-Akenine, Annick

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Thr Thr Lys Glu Leu Tyr Ala Gly Met Pro Thr Ile Gln Ile Thr Ala	
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ctt gaa aag att aca aaa cca ttt ttt gca gcc ata tca gat gaa aaa	3478
Leu Glu Lys Ile Thr Lys Pro Phe Phe Ala Ala Ile Ser Asp Glu Lys	
1110 1115 1120	
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Val Gln Gln Lys Leu Leu Arg Met Leu Phe Asp Leu Leu Val Asn Cys	
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Lys Asn Ser His Cys Ala Gln Thr Val Ser Ser Val Phe Lys Gly Ile	
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tcc gtt aat gct gaa caa gtc cga ata gaa ctg gag cca cca gat aaa	3622
Ser Val Asn Ala Glu Gln Val Arg Ile Glu Leu Glu Pro Pro Asp Lys	
1155 1160 1165 1170	
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Ala Lys Pro Leu Gly Thr Val Gln Gln Lys Arg Arg Gln Lys Met Gln	
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Gln Lys Lys Ser Gln Asp Leu Glu Ser Val Gln Glu Val Gly Gly Ser	
1190 1195 1200	
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Tyr Trp Gln Arg Val Thr Leu Ile Leu Glu Leu Leu Gln His Lys Lys	
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aag ctc aga agt cct cag ata ttg gtg cca act ctt ttt aac ttg cta	3814
Lys Leu Arg Ser Pro Gln Ile Leu Val Pro Thr Leu Phe Asn Leu Leu	
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tca aga tgt tta gaa ccc ttg cca caa gag cag gga aat atg gaa tac	3862
Ser Arg Cys Leu Glu Pro Leu Pro Gln Glu Gln Gly Asn Met Glu Tyr	
1235 1240 1245 1250	
acc aaa caa tta att ctt agt tgt ctg ctc aac atc tgc caa aaa cta	3910
Thr Lys Gln Leu Ile Leu Ser Cys Leu Leu Asn Ile Cys Gln Lys Leu	

tct cca gat ggt ggc aaa ata ccc aaa gat att tta gat gag gag aag	1255	1260	1265	3958
Ser Pro Asp Gly Gly Lys Ile Pro Lys Asp Ile Leu Asp Glu Glu Lys				
ttc aac gtg gag ttg ata gtt cag tgc atc cgc ctt tcg gag atg ccg	1270	1275	1280	4006
Phe Asn Val Glu Leu Ile Val Gln Cys Ile Arg Leu Ser Glu Met Pro				
cag acc cat cac cat gcc ctt tta ctt ttg ggc act gtt gct gga ata	1285	1290	1295	4054
Gln Thr His His His Ala Leu Leu Leu Leu Gly Thr Val Ala Gly Ile				
ttt ccg gat aaa gtt tta cac aat atc atg tct att ttt aca ttt atg	1300	1305	1310	4102
Phe Pro Asp Lys Val Leu His Asn Ile Met Ser Ile Phe Thr Phe Met				
gga gcc aat gtc atg cgc cta gat gat act tac agt ttt caa gtt att	1315	1320	1325	4150
Gly Ala Asn Val Met Arg Leu Asp Asp Thr Tyr Ser Phe Gln Val Ile				
aac aag aca gtg aaa atg gtt att ccc gca ctt att cag tct gat agt	1335	1340	1345	4198
Asn Lys Thr Val Lys Met Val Ile Pro Ala Leu Ile Gln Ser Asp Ser				
gga gat tct ata gaa gtt tca aga aac gtt gaa gag att gtg gta aaa	1350	1355	1360	4246
Gly Asp Ser Ile Glu Val Ser Arg Asn Val Glu Glu Ile Val Val Lys				
atc att agt gta ttt gtg gat gcg ctg cca cac gtc ccg gag cac agg	1365	1370	1375	4294
Ile Ile Ser Val Phe Val Asp Ala Leu Pro His Val Pro Glu His Arg				
cgc ctg ccc atc ctt gtt caa ctt gtt gat aca ctg ggt gca gag aaa	1380	1385	1390	4342
Arg Leu Pro Ile Leu Val Gln Leu Val Asp Thr Leu Gly Ala Glu Lys				
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Phe Leu Trp Ile Leu Leu Ile Leu Leu Phe Glu Gln Tyr Val Thr Lys				
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Thr Val Leu Ala Ala Ala Tyr Gly Glu Lys Asp Ala Ile Leu Glu Ala				
gac act gaa ttt tgg ttt tca gtc tgt tgt gag ttt agt gtc cag cat	1430	1435	1440	4486
Asp Thr Glu Phe Trp Phe Ser Val Cys Cys Glu Phe Ser Val Gln His				
cag ata caa agc ttg atg aat atc ctc cag tac tta cta aag ctg cca	1445	1450	1455	4534
Gln Ile Gln Ser Leu Met Asn Ile Leu Gln Tyr Leu Leu Lys Leu Pro				
gag gaa aaa gaa gaa acc att ccc aaa gca gtg tca ttt aat aag agt	1460	1465	1470	4582
Glu Glu Lys Glu Glu Thr Ile Pro Lys Ala Val Ser Phe Asn Lys Ser				
gaa tca caa gaa gaa atg cta cag gtt ttt aat gta gag act cac act	1475	1480	1485	4630
Glu Ser Gln Glu Glu Met Leu Gln Val Phe Asn Val Glu Thr His Thr				
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Ser Lys Gln Leu Arg His Phe Lys Phe Leu Ser Val Ser Phe Met Ser				
cag ctc ctg tct tcc aat aat ttt ctg aaa aag gta gtt gag agt ggt	1510	1515	1520	4726
Gln Leu Leu Ser Ser Asn Asn Phe Leu Lys Lys Val Val Glu Ser Gly				
ggt cct gag att tta aaa ggc ctt gaa gag agg ttg ctg gag acc gtt	1525	1530	1535	4774
Gly Pro Glu Ile Leu Lys Gly Leu Glu Glu Arg Leu Leu Glu Thr Val				
ctc ggc tat atc agt gca gtt gca cag tcc atg gaa agg aac gca gac	1540	1545	1550	4822
Leu Gly Tyr Ile Ser Ala Val Ala Gln Ser Met Glu Arg Asn Ala Asp				
aaa ctc acc gtg aag ttc tgg cgc gcg ctc ctt agt aaa gct tac gac	1555	1560	1565	4870
Lys Leu Thr Val Lys Phe Trp Arg Ala Leu Leu Ser Lys Ala Tyr Asp				
ctg tta gat aag gtc aat gcc ttg ctg ccc aca gag aca ttc att cct	1575	1580	1585	4918

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Lys	Thr	Ile	Val	Thr	Arg	Phe	Leu	Lys	Leu	Val	Pro	Asp	Leu	Leu	Ala		
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Ala	Glu	Asn	Pro	Asp	Pro	Phe	Val	Pro	Val	Leu	Xaa	Thr	Ala	Val	Lys		
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Pro	Gln	Leu	Pro	Ser	Leu	Met	Pro	Ser	Leu	Leu	Thr	Thr	Met	Lys	Asn		
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Glu	Met	Gly	Ser	Ala	Ser	Gln	Ala	Asn	Ile	Arg	Leu	Thr	Ser	Leu	Lys		
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Lys	Thr	Leu	Ala	Thr	Thr	Leu	Ala	Pro	Arg	Val	Leu	Leu	Pro	Ala	Ile		
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Leu Ala Asp Cys Ile Ala Glu Lys Leu Lys Gly Leu Phe Thr Leu Phe	
1940 1945 1950	
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Ala Gly His Leu Val Lys Pro Phe Ala Asp Thr Leu Xaa Gln Val Asn	
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Ile Ser Lys Thr Asp Glu Ala Phe Phe Asp Ser Glu Asn Asp Pro Glu	
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Lys Cys Cys Leu Leu Leu Gln Phe Ile Leu Asn Cys Leu Tyr Lys Ile	
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Gln Phe Ser Val Ala Met Ala Asp Asp Ser Leu Trp Lys Pro Leu Asn	
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Tyr Gln Ile Leu Leu Lys Thr Arg Asp Ser Ser Pro Lys Val Arg Phe	
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Ala Ala Leu Ile Thr Val Leu Ala Leu Ala Glu Lys Leu Lys Glu Asn	
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Met Thr

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Thr	Lys	Ala	Val	Asn	Lys	Gln	Leu	Asp	Glu	Asn	Ile	Ser	Leu	Phe	Leu		
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Ile	His	Leu	Ser	Pro	Tyr	Phe	Leu	Leu	Lys	Pro	Ala	Gln	Lys	Cys	Leu		
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Phe	Pro	Tyr	Ile	Gln	Lys	Gly	Leu	Lys	Ser	Ser	Leu	Pro	Asp	Tyr	Arg		
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gaa	act	tac	gat	gtc	agt	cct	ctt	ctg	cgt	tac	atg	ctt	ccc	cat	ctg	1174	
Glu	Thr	Tyr	Asp	Val	Ser	Pro	Leu	Leu	Arg	Tyr	Met	Leu	Pro	His	Leu		
			340			345					350						
gtc	gtc	tcc	atc	att	cat	cat	gtt	aca	qga	qaa	qaa	act	qaa	qga	atg	1222	

Val	Val	Ser	Ile	Ile	His	His	Val	Thr	Gly	Glu	Glu	Thr	Glu	Gly	Met	
355					360					365					370	
gat	ggg	caa	atc	tac	aag	aga	cac	tta	gaa	gct	ata	ctt	aca	aaa	ata	1270
Asp	Gly	Gln	Ile	Tyr	Lys	Arg	His	Leu	Glu	Ala	Ile	Leu	Thr	Lys	Ile	
			375						380					385		
tca	ctg	aag	aac	aac	tta	gac	cat	ttg	ttg	gct	agc	ctt	cta	ttt	gaa	1318
Ser	Leu	Lys	Asn	Asn	Leu	Asp	His	Leu	Leu	Ala	Ser	Leu	Leu	Phe	Glu	
			390					395					400			
gag	tat	att	tca	tat	agt	tca	cag	gaa	gaa	atg	gat	tct	aat	aaa	gtg	1356
Glu	Tyr	Ile	Ser	Tyr	Ser	Ser	Gln	Glu	Glu	Met	Asp	Ser	Asn	Lys	Val	
		405					410					415				
tct	ttg	ctt	aat	gaa	caa	ttt	ctt	cca	ctc	att	aga	ctt	tta	gaa	agc	1414
Ser	Leu	Leu	Asn	Glu	Gln	Phe	Leu	Pro	Leu	Ile	Arg	Leu	Leu	Glu	Ser	
		420				425					430					
aaa	tac	ccc	aga	aca	tta	gat	gtt	gta	tta	gag	gaa	cac	tta	aag	gaa	1462
Lys	Tyr	Pro	Arg	Thr	Leu	Asp	Val	Val	Leu	Glu	Glu	His	Leu	Lys	Glu	
435					440					445					450	
att	gca	gat	ctg	aaa	aaa	caa	gag	ctt	ttc	cat	cag	ttt	gtt	tct	ctt	1510
Ile	Ala	Asp	Leu	Lys	Lys	Gln	Glu	Leu	Phe	His	Gln	Phe	Val	Ser	Leu	
			455					460					465			
tct	aca	agt	gga	gga	aag	tat	cag	ttt	tta	gca	gat	tct	gat	act	tct	1558
Ser	Thr	Ser	Gly	Gly	Lys	Tyr	Gln	Phe	Leu	Ala	Asp	Ser	Asp	Thr	Ser	
		470					475					480				
ttg	atg	ctc	agc	ctg	aat	cat	cca	ctt	gct	cct	gtg	aga	att	ctg	gcc	1606
Leu	Met	Leu	Ser	Leu	Asn	His	Pro	Leu	Ala	Pro	Val	Arg	Ile	Leu	Ala	
		485					490					495				
atg	aat	cat	ttg	aaa	aag	atc	atg	aaa	aca	tca	aag	gag	ggg	gtt	gat	1654
Met	Asn	His	Leu	Lys	Lys	Ile	Met	Lys	Thr	Ser	Lys	Glu	Gly	Val	Asp	
	500					505					510					
gaa	tct	ttc	ata	aaa	gaa	gct	gtt	tta	gcc	cga	tta	ggg	gat	gat	aat	1702
Glu	Ser	Phe	Ile	Lys	Glu	Ala	Val	Leu	Ala	Arg	Leu	Gly	Asp	Asp	Asn	
515				520					525						530	
ata	gat	gtt	gtt	ttg	tcg	gct	ata	agt	gct	ttt	gag	att	ttc	aaa	gaa	1750
Ile	Asp	Val	Val	Leu	Ser	Ala	Ile	Ser	Ala	Phe	Glu	Ile	Phe	Lys	Glu	
			535					540					545			
cac	ttc	agt	tca	gaa	gtg	acg	att	tca	aat	ctt	ctg	aat	ctc	ttt	caa	1798
His	Phe	Ser	Ser	Glu	Val	Thr	Ile	Ser	Asn	Leu	Leu	Asn	Leu	Phe	Gln	
		550					555					560				
aga	gca	gaa	ctt	tca	aag	aat	gga	gaa	tgg	tac	gag	gta	ctt	aag	ata	1846
Arg	Ala	Glu	Leu	Ser	Lys	Asn	Gly	Glu	Trp	Tyr	Glu	Val	Leu	Lys	Ile	
		565					570					575				
gcc	gct	gac	ata	tta	att	aaa	gaa	gag	ata	ctg	agt	gaa	aat	gat	cag	1894
Ala	Ala	Asp	Ile	Leu	Ile	Lys	Glu	Glu	Ile	Leu	Ser	Glu	Asn	Asp	Gln	
	580					585					590					
ttg	tca	aat	cag	gtg	gtt	gta	tgt	ttg	ctg	cca	ttt	gtg	gtt	atc	aat	1942
Leu	Ser	Asn	Gln	Val	Val	Val	Cys	Leu	Leu	Pro	Phe	Val	Val	Ile	Asn	
595				600						605					610	
aat	gat	gat	acg	gaa	tct	gct	gag	atg	aaa	att	gct	ata	tat	tta	tca	1990
Asn	Asp	Asp	Thr	Glu	Ser	Ala	Glu	Met	Lys	Ile	Ala	Ile	Tyr	Leu	Ser	
			615					620					625			
aaa	tca	gga	atc	tgc	tcc	ctg	cac	cct	cta	tta	aga	ggc	tgg	gaa	gaa	2038
Lys	Ser	Gly	Ile	Cys	Ser	Leu	His	Pro	Leu	Leu	Arg	Gly	Trp	Glu	Glu	
		630					635					640				
gct	ctt	gaa	aat	gta	att	aaa	agc	aca	aag	cca	gga	aaa	cta	atc	ggg	2086
Ala	Leu	Glu	Asn	Val	Ile	Lys	Ser	Thr	Lys	Pro	Gly	Lys	Leu	Ile	Gly	
		645					650					655				
gta	gca	aat	cag	aag	atg	att	gag	ttg	ttg	gct	gat	aat	ata	aat	tta	2134
Val	Ala	Asn	Gln	Lys	Met	Ile	Glu	Leu	Leu	Ala	Asp	Asn	Ile	Asn	Leu	
		650				665					670					
gga	gat	cct	tct	tca	atg	tta	aag	atg	gtg	gag	gat	ttg	ata	agc	gtg	2182
Gly	Asp	Pro	Ser	Ser	Met	Leu	Lys	Met	Val	Glu	Asp	Leu	Ile	Ser	Val	
675					680					685					690	

ggt gag gag gag tcc ttt aac ctg aag cag aaa gta acg ttt cat gtg	2230
Gly Glu Glu Glu Ser Phe Asn Leu Lys Gln Lys Val Thr Phe His Val	
695 700 705	
atc ctg tct gtg ctc gtc tct tgt tgt tca tct tta aaa gaa acc cac	2278
Ile Leu Ser Val Leu Val Ser Cys Cys Ser Ser Leu Lys Glu Thr His	
710 715 720	
ttt cca ttt gcg ata aga gtc ttc agt ttg ttg cag aaa aaa ata aag	2326
Phe Pro Phe Ala Ile Arg Val Phe Ser Leu Leu Gln Lys Lys Ile Lys	
725 730 735	
aag ctt gaa agt gtc att act gca gtg gaa atc ccc tca gaa tgg cac	2374
Lys Leu Glu Ser Val Ile Thr Ala Val Glu Ile Pro Ser Glu Trp His	
740 745 750	
att gaa ctg atg tta gac aga ggg atc cca gta gag ctg tgg gca cat	2422
Ile Glu Leu Met Leu Asp Arg Gly Ile Pro Val Glu Leu Trp Ala His	
755 760 765 770	
tat gta gaa gag ctc aac agc act cag agg gtg gcc gtg gag gac tcg	2470
Tyr Val Glu Glu Leu Asn Ser Thr Gln Arg Val Ala Val Glu Asp Ser	
775 780 785	
gtt ttt ctt gta ttt tcc ttg aaa aaa ttt att tat gca ctg aaa gct	2518
Val Phe Leu Val Phe Ser Leu Lys Lys Phe Ile Tyr Ala Leu Lys Ala	
790 795 800	
cct aaa tct ttt cct aaa ggt gat ata tgg tgg aat cct gaa caa ctg	2566
Pro Lys Ser Phe Pro Lys Gly Asp Ile Trp Trp Asn Pro Glu Gln Leu	
805 810 815	
aaa gaa gac agc agg gac tat ctg cac ttg ctc att ggg ctg ttt gag	2614
Lys Glu Asp Ser Arg Asp Tyr Leu His Leu Leu Ile Gly Leu Phe Glu	
820 825 830	
atg atg ctc aat ggt gcc gat gct gtt cat ttc aga gtt ctg atg aaa	2662
Met Met Leu Asn Gly Ala Asp Ala Val His Phe Arg Val Leu Met Lys	
835 840 845 850	
ctt ttc ata aag gtk cat cta gaa gat gtt ttt cag tta ttc aag ttc	2710
Leu Phe Ile Lys Val His Leu Glu Asp Val Phe Gln Leu Phe Lys Phe	
855 860 865	
tgt tct gtt tta tgg acc tat ggt tct agc ctt tca aat cca cta aac	2758
Cys Ser Val Leu Trp Thr Tyr Gly Ser Ser Leu Ser Asn Pro Leu Asn	
870 875 880	
tgc agt gtg aaa aca gtg ctg cag act caa gct ctt tat gtg ggc tgt	2806
Cys Ser Val Lys Thr Val Leu Gln Thr Gln Ala Leu Tyr Val Gly Cys	
885 890 895	
gca atg ctt tct tct cag aag aca cag tgt aaa cac caa ctg gca tcc	2854
Ala Met Leu Ser Ser Gln Lys Thr Gln Cys Lys His Gln Leu Ala Ser	
900 905 910	
ata tct tct cca gtg gtg aca tct tta ctc att aac ctg gga agc ccc	2902
Ile Ser Ser Pro Val Val Thr Ser Leu Leu Ile Asn Leu Gly Ser Pro	
915 920 925 930	
gta aaa gaa gtt cgt agg gct gcc att cag tgt ctc cag gcc ctc agt	2950
Val Lys Glu Val Arg Arg Ala Ala Ile Gln Cys Leu Gln Ala Leu Ser	
935 940 945	
gga gtg gca tcc ccg ttt tat ctg ata ata gat cat ttg att tct aaa	2998
Gly Val Ala Ser Pro Phe Tyr Leu Ile Ile Asp His Leu Ile Ser Lys	
950 955 960	
gca gag gag atc act tca gat gct gcc tat gtt att cag gat ttg gct	3046
Ala Glu Glu Ile Thr Ser Asp Ala Ala Tyr Val Ile Gln Asp Leu Ala	
965 970 975	
act tta ttt gag gaa cta cag aga gaa aag aaa ctg aaa tct cat cag	3094
Thr Leu Phe Glu Glu Leu Gln Arg Glu Lys Lys Leu Lys Ser His Gln	
980 985 990	
aag ttg tct gaa act ttg aaa aac tta ctt agt tgt gtg tat agt tgc	3142
Lys Leu Ser Glu Thr Leu Lys Asn Leu Leu Ser Cys Val Tyr Ser Cys	
995 1000 1005 1010	
cca tct tat ata gca aaa gat ttg atg aaa gta ctt cag gga gtc aac	3190
Pro Ser Tyr Ile Ala Lys Asp Leu Met Lys Val Leu Gln Gly Val Asn	

ggt gag atg gtg ctt tct cag cta ttg cct atg gct gaa caa ctg cta	1015	1020	1025	3238
Gly Glu Met Val Leu Ser Gln Leu Leu Pro Met Ala Glu Gln Leu Leu				
gaa aag atc cag aag gag ccc aca gct gtg ctg aaa gat gag gcc atg	1030	1035	1040	3285
Glu Lys Ile Gln Lys Glu Pro Thr Ala Val Leu Lys Asp Glu Ala Met				
gtt ctg cat ctc act ctg gga aag tat aat gaa ttt tca gtt tcc ctt	1045	1050	1055	3334
Val Leu His Leu Thr Leu Gly Lys Tyr Asn Glu Phe Ser Val Ser Leu				
tta aat gag gat ccg aag agt cta gat ata ttt ata aaa gct gtg cac	1060	1065	1070	3382
Leu Asn Glu Asp Pro Lys Ser Leu Asp Ile Phe Ile Lys Ala Val His				
aca aca aag gaa ctt tac gcg gga atg cca acc att cag atc aca gcc	1075	1080	1085	3430
Thr Thr Lys Glu Leu Tyr Ala Gly Met Pro Thr Ile Gln Ile Thr Ala				
ctt gaa aag att aca aaa cca ttt ttt gca gcc ata tca gat gaa aaa	1095	1100	1105	3478
Leu Glu Lys Ile Thr Lys Pro Phe Phe Ala Ala Ile Ser Asp Glu Lys				
gtt cag cag aag ctt tta aga atg ttg ttt gat tta ttg gtg aac tgt	1110	1115	1120	3525
Val Gln Gln Lys Leu Leu Arg Met Leu Phe Asp Leu Leu Val Asn Cys				
aaa aac tca cat tgt gct cag act gtc agc agt gtt ttt aaa ggg att	1125	1130	1135	3574
Lys Asn Ser His Cys Ala Gln Thr Val Ser Ser Val Phe Lys Gly Ile				
tcc gtt aat gct gaa caa gtc cga ata gaa ctg gag cca cca gat aaa	1140	1145	1150	3622
Ser Val Asn Ala Glu Gln Val Arg Ile Glu Leu Glu Pro Pro Asp Lys				
gct aaa ccc ttg ggc aca gtt cag caa aaa aga agg caa aaa atg cag	1155	1160	1165	3670
Ala Lys Pro Leu Gly Thr Val Gln Gln Lys Arg Arg Gln Lys Met Gln				
cag aaa aaa tca caa gat cta gaa tct gtt cag gaa gtt gga ggt tct	1175	1180	1185	3718
Gln Lys Lys Ser Gln Asp Leu Glu Ser Val Gln Glu Val Gly Gly Ser				
tac tgg caa aga gta act ctc atc ctg gaa tta ctg cag cac aaa aag	1190	1195	1200	3766
Tyr Trp Gln Arg Val Thr Leu Ile Leu Glu Leu Leu Gln His Lys Lys				
aag ctc aga agt cct cag ata ttg gtg cca act ctt ttt aac ttg cta	1205	1210	1215	3814
Lys Leu Arg Ser Pro Gln Ile Leu Val Pro Thr Leu Phe Asn Leu Leu				
tca aga tgt tta gaa ccc ttg cca caa gag cag gga aat atg gaa tac	1220	1225	1230	3862
Ser Arg Cys Leu Glu Pro Leu Pro Gln Glu Gln Gly Asn Met Glu Tyr				
acc aaa caa tta att ctt agt tgt ctg ctc aac atc tgc caa aaa cta	1235	1240	1245	3910
Thr Lys Gln Leu Ile Leu Ser Cys Leu Leu Asn Ile Cys Gln Lys Leu				
tct cca gat ggt ggc aaa ata ccc aaa gat att tta gat gag gag aag	1255	1260	1265	3958
Ser Pro Asp Gly Gly Lys Ile Pro Lys Asp Ile Leu Asp Glu Glu Lys				
ttc aac gtg gag ttg ata gtt cag tgc atc cgc ctt tcg gag atg ccg	1270	1275	1280	4005
Phe Asn Val Glu Leu Ile Val Gln Cys Ile Arg Leu Ser Glu Met Pro				
cag acc cat cac cat gcc ctt tta ctt ttg ggc act gtt gct gga ata	1285	1290	1295	4054
Gln Thr His His His Ala Leu Leu Leu Leu Gly Thr Val Ala Gly Ile				
ttt ccg gat aaa gtt tta cac aat atc atg tct att ttt aca ttt atg	1300	1305	1310	4102
Phe Pro Asp Lys Val Leu His Asn Ile Met Ser Ile Phe Thr Phe Met				
gga gcc aat gtc atg cgc cta gat gat act tac agt ttt caa gtt att	1315	1320	1325	4150
Gly Ala Asn Val Met Arg Leu Asp Asp Thr Tyr Ser Phe Gln Val Ile				
aac aag aca gtg aaa atg gtt att ccc gca ctt att cag tct gat agt	1335	1340	1345	4198

Asn Lys Thr Val Lys Met Val Ile Pro Ala Leu Ile Gln Ser Asp Ser	
1350 1355 1360	
gga gat tct ata gaa gtt tca aga aac gtt gaa gag att gtg gta aaa	4245
Gly Asp Ser Ile Glu Val Ser Arg Asn Val Glu Glu Ile Val Val Lys	
1365 1370 1375	
atc att agt gta ttt gtg gat gcg ctg cca cac gtc ccg gag cac agg	4294
Ile Ile Ser Val Phe Val Asp Ala Leu Pro His Val Pro Glu His Arg	
1380 1385 1390	
cgc ctg ccc atc ctt gtt caa ctt gtt gat aca ctg ggt gca gag aaa	4342
Arg Leu Pro Ile Leu Val Gln Leu Val Asp Thr Leu Gly Ala Glu Lys	
1395 1400 1405 1410	
ttc ctc tgg att ctc ctc atc ttg ctt ttt gaa cag tat gtc aca aaa	4390
Phe Leu Trp Ile Leu Leu Ile Leu Leu Phe Glu Gln Tyr Val Thr Lys	
1415 1420 1425	
aca gtg ctg gcg gct gcc tat ggc gaa aag gat gct att tta gaa gca	4438
Thr Val Leu Ala Ala Ala Tyr Gly Glu Lys Asp Ala Ile Leu Glu Ala	
1430 1435 1440	
gac act gaa ttt tgg ttt tca gtc tgt tgt gag ttt agt gtc cag cat	4486
Asp Thr Glu Phe Trp Phe Ser Val Cys Cys Glu Phe Ser Val Gln His	
1445 1450 1455	
cag ata caa agc ttg atg aat atc ctc cag tac tta cta aag ctg cca	4534
Gln Ile Gln Ser Leu Met Asn Ile Leu Gln Tyr Leu Leu Lys Leu Pro	
1460 1465 1470	
gag gaa aaa gaa gaa acc att ccc aaa gca gtg tca ttt aat aag agt	4582
Glu Glu Lys Glu Glu Thr Ile Pro Lys Ala Val Ser Phe Asn Lys Ser	
1475 1480 1485 1490	
gaa tca caa gaa gaa atg cta cag gtt ttt aat gta gag act cac act	4630
Glu Ser Gln Glu Glu Met Leu Gln Val Phe Asn Val Glu Thr His Thr	
1495 1500 1505	
agc aag caa ctg cgg cat ttt aaa ttt ttg tca gtg tcc ttc atg tct	4678
Ser Lys Gln Leu Arg His Phe Lys Phe Leu Ser Val Ser Phe Met Ser	
1510 1515 1520	
cag ctc ctg tct tcc aat aat ttt ctg aaa aag gta gtt gag agt ggt	4726
Gln Leu Leu Ser Ser Asn Asn Phe Leu Lys Lys Val Val Glu Ser Gly	
1525 1530 1535	
ggt cct gag att tta aaa ggc ctt gaa gag agg ttg ctg gag acc gtt	4774
Gly Pro Glu Ile Leu Lys Gly Leu Glu Glu Arg Leu Leu Glu Thr Val	
1540 1545 1550	
ctc ggc tat atc agt gca gtt gca cag tcc atg gaa agg aac gca gac	4822
Leu Gly Tyr Ile Ser Ala Val Ala Gln Ser Met Glu Arg Asn Ala Asp	
1555 1560 1565 1570	
aaa ctc acc gtg aag ttc tgg cgc gcg ctc ctt agt aaa gct tac gac	4870
Lys Leu Thr Val Lys Phe Trp Arg Ala Leu Leu Ser Lys Ala Tyr Asp	
1575 1580 1585	
ctg tta gat aag gtc aat gcc ttg ctg ccc aca gag aca ttc att cct	4918
Leu Leu Asp Lys Val Asn Ala Leu Leu Pro Thr Glu Thr Phe Ile Pro	
1590 1595 1600	
gtg atc aga ggg ctg gtg ggc aat ccc ctg cca tct gtt cgc cgc aaa	4966
Val Ile Arg Gly Leu Val Gly Asn Pro Leu Pro Ser Val Arg Arg Lys	
1605 1610 1615	
gcg ctg gac ctt ttg aat aac aag ctg cag caa aat ata tcc tgg aag	5014
Ala Leu Asp Leu Leu Asn Asn Lys Leu Gln Gln Asn Ile Ser Trp Lys	
1620 1625 1630	
aag aca ata gtt acc cgt ttc cta aaa ctg gtt cca gac ctt ttg gcc	5062
Lys Thr Ile Val Thr Arg Phe Leu Lys Leu Val Pro Asp Leu Leu Ala	
1635 1640 1645 1650	
att gtg cag cgt aag aaa aag gaa ggg gaa gaa gaa caa gca atc aac	5110
Ile Val Gln Arg Lys Lys Lys Glu Gly Glu Glu Glu Gln Ala Ile Asn	
1655 1660 1665	
aga cag aca gcg ttg tat acc tta aag ctt tta tgc aag aat ttt ggt	5158
Arg Gln Thr Ala Leu Tyr Thr Leu Lys Leu Leu Cys Lys Asn Phe Gly	
1670 1675 1680	

gca gaa aat cca gat cct ttt gtc cca gtg ctg arc act gct gtg aaa	5206
Ala Glu Asn Pro Asp Pro Phe Val Pro Val Leu Xaa Thr Ala Val Lys	
1685 1690 1695	
ctg att gct cca gag aga aag gag gag aag aat gtc ytg gga agc gcg	5254
Leu Ile Ala Pro Glu Arg Lys Glu Glu Lys Asn Val Leu Gly Ser Ala	
1700 1705 1710	
ctg ctg tgc ata gca gag gtg acc tcc acc ctg gag gcg ctg gcc atc	5302
Leu Leu Cys Ile Ala Glu Val Thr Ser Thr Leu Glu Ala Leu Ala Ile	
1715 1720 1725 1730	
ccc cag ctt ccc agc ctg atg cca tcg ttg ctg aca aca atg aag aac	5350
Pro Gln Leu Pro Ser Leu Met Pro Ser Leu Thr Thr Met Lys Asn	
1735 1740 1745	
acc agc gag ctg gtc tcc agc gag gtc tac ctg ctc agt gcc ttg gct	5398
Thr Ser Glu Leu Val Ser Ser Glu Val Tyr Leu Leu Ser Ala Leu Ala	
1750 1755 1760	
gct ctg cag aag gtt gtg gag act ctc ccg cac ttc atc agc ccc tat	5446
Ala Leu Gln Lys Val Val Glu Thr Leu Pro His Phe Ile Ser Pro Tyr	
1765 1770 1775	
ctg gaa ggc att ctc tcc cag gtg att cat ctg gag aaa atc act agt	5494
Leu Glu Gly Ile Leu Ser Glu Val Ile His Leu Glu Lys Ile Thr Ser	
1780 1785 1790	
gaa atg ggt tct gcg tca cag gct aat atc cgt ctc aca tct ctt aaa	5542
Glu Met Gly Ser Ala Ser Gln Ala Asn Ile Arg Leu Thr Ser Leu Lys	
1795 1800 1805 1810	
aag aca ctg gct acc aca ctt gca ccc cga gtc ctg ttg ccc gcc atc	5590
Lys Thr Leu Ala Thr Thr Leu Ala Pro Arg Val Leu Leu Pro Ala Ile	
1815 1820 1825	
aaa aaa act tac aag cag att gag aag aac tgg aag aat cac atg ggt	5638
Lys Lys Thr Tyr Lys Gln Ile Glu Lys Asn Trp Lys Asn His Met Gly	
1830 1835 1840	
ccg ttt atg agc atc ttg caa gag cat att ggg gyg atg aag aag gaa	5686
Pro Phe Met Ser Ile Leu Gln Glu His Ile Gly Xaa Met Lys Lys Glu	
1845 1850 1855	
gag ctc acc tcc cat cag tct cag cta acc gcc ttt ttc ctg gar gcc	5734
Glu Leu Thr Ser His Gln Ser Gln Leu Thr Ala Phe Phe Leu Glu Ala	
1860 1865 1870	
ctg gac ttc cga gcc cag cac tct gag aac gat ctg gag gaa gtt gga	5782
Leu Asp Phe Arg Ala Gln His Ser Glu Asn Asp Leu Glu Glu Val Gly	
1875 1880 1885 1890	
aaa acg gaa aat tgt atc att gac tgt cta gta gcc atg gtt gtc aaa	5830
Lys Thr Glu Asn Cys Ile Ile Asp Cys Leu Val Ala Met Val Val Lys	
1895 1900 1905	
ctt tcc gag gtc aca ttc agg ccc ctg ttc ttc aag ctg ttt gat tgg	5878
Leu Ser Glu Val Thr Phe Arg Pro Leu Phe Phe Lys Leu Phe Asp Trp	
1910 1915 1920	
gct aaa aca gaa gat gcc cca aag gac agg ttg ttg aca ttt tac aac	5926
Ala Lys Thr Glu Asp Ala Pro Lys Asp Arg Leu Leu Thr Phe Tyr Asn	
1925 1930 1935	
ttg gca gat tgc att gct gaa aag ctg aaa ggg ctt ttt act ctg ttt	5974
Leu Ala Asp Cys Ile Ala Glu Lys Leu Lys Gly Leu Phe Thr Leu Phe	
1940 1945 1950	
gcc ggc cac tta gtg aag cct ttt gct gac acc ttg rac cag gtg aac	6022
Ala Gly His Leu Val Lys Pro Phe Ala Asp Thr Leu Xaa Gln Val Asn	
1955 1960 1965 1970	
atc tcc aaa aca gat gaa gca ttt ttt gac tct gaa aat gac cct gaa	6070
Ile Ser Lys Thr Asp Glu Ala Phe Phe Asp Ser Glu Asn Asp Pro Glu	
1975 1980 1985	
aag tgc tgc ttg ctg ttg cag ttt att ttg aac tgt tta tac aaa atc	6118
Lys Cys Cys Leu Leu Gln Phe Ile Leu Asn Cys Leu Tyr Lys Ile	
1990 1995 2000	
ttc ctt ttt gat acc cag cat ttt ata agt aaa gag aga gca gra gcc	6166
Phe Leu Phe Asp Thr Gln His Phe Ile Ser Lys Glu Arg Ala Xaa Ala	

2005	2010	2015	
ttg atg atg cct ctg gtg gat cag ctg gaa aac	agg ctt ggg gga gaa	6214	
Leu Met Met Pro Leu Val Asp Gln Leu Glu Asn	Arg Leu Gly Gly Glu		
2020	2025	2030	
gag aaa ttc cag gaa cgg gtg aca aag cac ctg	ata cca tgc atc gca	6252	
Glu Lys Phe Gln Glu Arg Val Thr Lys His Leu	Ile Pro Cys Ile Ala		
2035	2040	2045	2050
cag ttt tcr gtg gcc atg gcg gat gac tct ctt	tgg aaa cca ctg aac	6310	
Gln Phe Ser Val Ala Met Ala Asp Asp Ser Leu	Trp Lys Pro Leu Asn		
2055	2060	2065	
tac cag att ctg cta aag acg aga gac tcc tcg	cct aag gtt cga ttt	6358	
Tyr Gln Ile Leu Leu Lys Thr Arg Asp Ser Ser	Pro Lys Val Arg Phe		
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Tyr Ile Val Leu Leu Pro Glu Ser Ile Pro Phe	Leu Ala Glu Leu Met		
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Gln Leu Glu Thr Val Leu Gly Glu Pro Leu Gln	Ser Tyr Phe *		
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 Phe Leu Ile His Leu Ser Pro Tyr Phe Leu Leu Lys Pro Ala Gln Lys
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 Cys Leu Glu Trp Leu Ile His Arg Phe His Ile His Leu Tyr Asn Gln
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Ser	Val	Gly	Glu	Glu	Glu	Ser	Phe	Asn	Leu	Lys	Gln	Lys	Val	Thr	Phe		
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Thr	His	Phe	Pro	Phe	Ala	Ile	Arg	Val	Phe	Ser	Leu	Leu	Gln	Lys	Lys		
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Trp	His	Ile	Glu	Leu	Met	Leu	Asp	Arg	Gly	Ile	Pro	Val	Glu	Leu	Trp		
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Ala	His	Tyr	Val	Glu	Glu	Leu	Asn	Ser	Thr	Gln	Arg	Val	Ala	Val	Glu		
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785					790					795					800		
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Phe	Glu	Met	Met	Leu	Asn	Gly	Ala	Asp	Ala	Val	His	Phe	Arg	Val	Leu		
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Ser	Pro	Val	Lys	Glu	Val	Arg	Arg	Ala	Ala	Ile	Gln	Cys	Leu	Gln	Ala		
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Ser	Leu	Leu	Asn	Glu	Asp	Pro	Lys	Ser	Leu	Asp	Ile	Phe	Ile	Lys	Ala		
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Val	His	Thr	Thr	Lys	Glu	Leu	Tyr	Ala	Gly	Met	Pro	Thr	Ile	Gln	Ile		
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Met Gln Gln Lys Lys Ser Gln Asp Leu Glu Ser Val Gln Glu Val Gly		
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Lys Lys Lys Leu Arg Ser Pro Gln Ile Leu Val Pro Thr Leu Phe Asn		
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Val Ile Asn Lys Thr Val Lys Met Val Ile Pro Ala Leu Ile Gln Ser		
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Ser Ala Leu Leu Cys	Ile Ala Glu Val	Thr Ser Thr Leu	Glu Ala Leu	
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Leu Lys Lys Thr Leu	Ala Thr Thr Leu	Ala Pro Arg Val	Leu Leu Pro	
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Pro Glu Lys Cys Cys	Leu Leu Leu Gln	Phe Ile Leu Asn	Cys Leu Tyr	
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agaagctgga	aaagaatg	atg ttg tcc tta aac aac	cta cag aat atc atc			231									
		Met Leu Ser Leu Asn Asn	Leu Gln Asn Ile Ile												
		1 5	10												
tat aac ccg gta atc ccg tat gtt ggc acc att ccc gat cag ctg gat						279									
Tyr Asn Pro Val Ile Pro Tyr Val Gly Thr Ile Pro Asp Gln Leu Asp															
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cct gga act ttg att gtg ata tgt ggg cat gtt cct agt gac gca gac						327									
Pro Gly Thr Leu Ile Val Ile Cys Gly His Val Pro Ser Asp Ala Asp															
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aga ttc cag gtg gat ctg cag aat ggc agc agt gtg aaa cct cga gcc						375									
Arg Phe Gln Val Asp Leu Gln Asn Gly Ser Ser Val Lys Pro Arg Ala															
	45	50	55												
gat gtg gcc ttt cat ttc aat cct cgt ttc aaa agg gcc ggc tgc att						423									
Asp Val Ala Phe His Phe Asn Pro Arg Phe Lys Arg Ala Gly Cys Ile															
60	65	70	75												
gtt tgc aat act ttg ata aat gaa aaa tgg gga cgg gaa gag atc acc						471									
Val Cys Asn Thr Leu Ile Asn Glu Lys Trp Gly Arg Glu Glu Ile Thr															
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tat gac acg cct ttc aaa aga gaa aag tct ttt gag atc gtg att atg						519									
Tyr Asp Thr Pro Phe Lys Arg Glu Lys Ser Phe Glu Ile Val Ile Met															
	95	100	105												
gtg cta aag gac aaa ttc cag gtg gct gta aat gga aaa cat act ctg						567									
Val Leu Lys Asp Lys Phe Gln Val Ala Val Asn Gly Lys His Thr Leu															
	110	115	120												
ctc tat ggc cac agg atc ggc cca gag aaa ata gac act ctg ggc att						615									
Leu Tyr Gly His Arg Ile Gly Pro Glu Lys Ile Asp Thr Leu Gly Ile															

125	130	135	
tat ggc aaa gtg aat att	cac tca att ggt ttt	agc ttc agc tcg gac	563
Tyr Gly Lys Val Asn Ile	His Ser Ile Gly Phe	Ser Phe Ser Ser Asp	
140	145	150	155
tta caa agt acc caa gca	tct agt ctg gaa ctg	aca gag ata agt aga	711
Leu Gln Ser Thr Gln Ala	Ser Ser Leu Glu Leu	Thr Glu Ile Ser Arg	
160	165	170	
gaa aat gtt cca aag tct	ggc acg ccc cag ctt	agc ctg cca ttc gct	759
Glu Asn Val Pro Lys Ser	Gly Thr Pro Gln Leu	Ser Leu Pro Phe Ala	
175	180	185	
gca agg ttg aac acc ccc	atg ggc cct gga cga	act gtc gtt aaa	807
Ala Arg Leu Asn Thr Pro	Met Gly Pro Gly Arg	Thr Val Val Val Lys	
190	195	200	
gga gaa gtg aat gca aat	gcc aaa agc ttt aat	gtt gac cta cta gca	855
Gly Glu Val Asn Ala Asn	Ala Lys Ser Phe Asn	Val Asp Leu Leu Ala	
205	210	215	
gga aaa tca aag gat att	gct cta cac ttg aac	cca cgc ctg aat att	903
Gly Lys Ser Lys Asp Ile	Ala Leu His Leu Asn	Pro Arg Leu Asn Ile	
220	225	230	235
aaa gca ttt gta aga aat	tct ttt ctt cag gag	tcc tgg gga gaa gaa	951
Lys Ala Phe Val Arg Asn	Ser Phe Leu Gln Glu	Ser Trp Gly Glu Glu	
240	245	250	
gag aga aat att acc tct	ttc cca ttt agt cct	ggg atg tac ttt gag	999
Glu Arg Asn Ile Thr Ser	Phe Pro Phe Ser Pro	Gly Met Tyr Phe Glu	
255	260	265	
atg ata att tac tgt gat	gtt aga gaa ttc aag	gtt gca gta aat ggc	1047
Met Ile Ile Tyr Cys Asp	Val Arg Glu Phe Lys	Val Ala Val Asn Gly	
270	275	280	
gta cac agc ctg gag tac	aaa cac aga ttt aaa	gag ctc agc agt att	1095
Val His Ser Leu Glu Tyr	Lys His Arg Phe Lys	Glu Leu Ser Ser Ile	
285	290	295	
gac acg ctg gaa att aat	gga gac atc cac tta	ctg gaa caa tca ttc	1143
Asp Thr Leu Glu Ile Asn	Gly Asp Ile His Leu	Leu Glu Gln Ser Phe	
300	305	310	315
aat caa aag agt gaa atg	aag cac att aac aaa	gca gga ggc gcc acg	1191
Asn Gln Lys Ser Glu Met	Lys His Ile Asn Lys	Ala Gly Gly Ala Thr	
320	325	330	
gac cgc ctc cct cca cac	cgc tcc ttc cgc ctt	cat tcc ttg ccc aca	1239
Asp Arg Leu Pro Pro His	Arg Ser Phe Arg Leu	His Ser Leu Pro Thr	
335	340	345	
ggc ttg cac tgg aag ctg	aat aag aat ccc caa	aac tca aac ttc cta	1287
Gly Leu His Trp Lys Leu	Asn Lys Asn Pro Gln	Asn Ser Asn Phe Leu	
350	355	360	
ggg atg cca ccc ctt tag	tagctcacac ctccccctc	caagagctaa	1335
Gly Met Pro Pro Leu *			
365			
gaaacaaagg agaatgtact	tttgtagctt agataagcaa	tgaatcagta aaggactgat	1395
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acggactctc aaatgatcag	gaggtgggtca cttcgcaact	tgctccctcc acccaactca	1875
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aactgctagt cacgttatat	ccaaatctgc attatcattg	ggcacatttt cacagaattt	1995
tactgaatta ttcccttaatt	gtttaatggt tgggaatagt	ttgggaatta ccttccatca	2055
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ctttcatctt	agaataccag	tttcaccatt	tgggagctgt	ttgtaatatg	tgcaacctta	2355
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aaatgaacca	gtggtgggga	ggaagtgggt	gaggtgtagg	tgaaacaaga	ttggccacgt	180
cgataattgc	tggagctggg	cgatgaaagc	acagttctag	aagcttgttt	ctcccacctg	240
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 <213> Homo sapiens

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cctggtcctg	aaaagtccca	gccccgagcg	ccctccctcc	tagacctgga	ggcctggaac	180
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aacctgctcc	gtggagcgcc	tgaaacacca	gtctttgggg	ccagtgcctc	agtttcaatc	300
caggtaacct	ttaaataaaa	cttgccctaaa	atcttaggtc	atacacagaa	gagactccaa	360
tcgacaagaa	gctggaaaag	aatg atg	ttg tcc	tta aac	aac cta	cag aat
		Met	Leu	Ser	Leu	Asn Asn Leu Gln Asn
		1			5	
atc atc	tat aac	ccg gta	atc ccg	tat gtt	ggc acc	att ccc
Ile Ile	Tyr Asn	Pro Val	Ile Pro	Tyr Val	Gly Thr	Ile Pro
10		15		20		25
ctg gat	cct gga	act ttg	att gtg	ata tgt	ggg cat	gtt cct
Leu Asp	Pro Gly	Thr Leu	Ile Val	Ile Cys	Gly His	Val Pro
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Ala Asp						
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<210> 11
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 <212> DNA
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<220>
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<220>
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tcttaggtca	tacacagaag	agactccaat	cgacaagaag	ctggaaaaga	atg atg	176

Met

1

ttg tcc tta	aac aac cta	cag aat atc	atc tat aac	ccg gta atc	ccg	224
Leu Ser Leu	Asn Asn Leu	Gln Asn Ile	Ile Tyr Asn	Pro Val Ile	Pro	

5

10

15

tat gtt ggc	acc att ccc	gat cag ctg	gat cct gga	act ttg	att gtg	272
Tyr Val Gly	Thr Ile Pro	Asp Gln Leu	Asp Pro Gly	Thr Leu	Ile Val	

20

25

30

ata tgt ggg	cat gtt cct	agt gac gca	gac ag			304
Ile Cys Gly	His Val Pro	Ser Asp Ala	Asp			

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<211> 473

<212> DNA

<213> Homo sapiens

<220>

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<221> CDS

<222> 343..473

<400> 12

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ggaagcagat	gtatgtataa	ggatccgccc	acggacgcca	gagccgggaa	ccctgacggc	180
acttagctgc	tgacaaacaa	cctgctccgt	ggagcgcttg	aaacaccagt	ctttggggcc	240
agtgcctcag	tttcaatcca	ggtaaccttt	aaatgaaact	tgcttaaaat	cttaggtcat	300
acacagaaga	gactccaatc	gacaagaagc	tggaaaagaa	tg atg ttg	tcc tta	354

Met Leu Ser Leu

1

aac aac cta	cag aat atc	atc tat aac	ccg gta atc	ccg tat gtt	ggc	402
Asn Asn Leu	Gln Asn Ile	Ile Tyr Asn	Pro Val Ile	Pro Tyr Val	Gly	

5

10

15

20

acc att ccc	gat cag ctg	gat cct gga	act ttg att	gtg ata tgt	ggg	450
Thr Ile Pro	Asp Gln Leu	Asp Pro Gly	Thr Leu Ile	Val Ile Cys	Gly	

25

30

35

cat gtt cct	agt gac gca	gac ag				473
His Val Pro	Ser Asp Ala	Asp				

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<210> 13

<211> 2077

<212> DNA

<213> Homo sapiens

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<221> 5'UTR

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<221> 3'UTR

<222> 914..2077

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caacctgctc	cgtggagcgc	ctgaaacacc	agtctttggg	gccagtgcct	cagtttcaat	180
ccaggtaacc	tttaaataaa	acttgccctaa	aatcttaggt	catacacaga	agagactcca	240
atcgacaaga	agctggaaaa	gaatg	atg ttg tcc tta	aac aac cta cag aat		292
		Met	Leu Ser Leu	Asn Asn Leu Gln Asn		
		1		5		
atc atc tat aac ccg gta atc ccg tat gtt ggc acc att ccc gat cag						340
Ile Ile Tyr Asn Pro Val Ile Pro Tyr Val Gly Thr Ile Pro Asp Gln						
10	15		20		25	
ctg gat cct gga act ttg att gtg ata tgt ggg cat gtt cct agt gac						388
Leu Asp Pro Gly Thr Leu Ile Val Ile Cys Gly His Val Pro Ser Asp						
	30		35		40	
gca gac aga ttc cag gtg gat ctg cag aat ggc agc agt gtg aaa cct						436
Ala Asp Arg Phe Gln Val Asp Leu Gln Asn Gly Ser Ser Val Lys Pro						
	45		50		55	
cga gcc gat gtg gcc ttt cat ttc aat cct cgt ttc aaa agg gcc ggc						484
Arg Ala Asp Val Ala Phe His Phe Asn Pro Arg Phe Lys Arg Ala Gly						
	60		65		70	
tgc att gtt tgc aat act ttg ata aat gaa aaa tgg gga cgg gaa gag						532
Cys Ile Val Cys Asn Thr Leu Ile Asn Glu Lys Trp Gly Arg Glu Glu						
	75		80		85	
atc acc tat gac acg cct ttc aaa aga gaa aag tct ttt gag atc gtg						580
Ile Thr Tyr Asp Thr Pro Phe Lys Arg Glu Lys Ser Phe Glu Ile Val						
	90		95		100	105
att atg gtg cta aag gac aaa ttc cag atg ata att tac tgt gat gtt						628
Ile Met Val Leu Lys Asp Lys Phe Gln Met Ile Ile Tyr Cys Asp Val						
	110		115		120	
aga gaa ttc aag gtt gca gta aat ggc gta cac agc ctg gag tac aaa						676
Arg Glu Phe Lys Val Ala Val Asn Gly Val His Ser Leu Glu Tyr Lys						
	125		130		135	
cac aga ttt aaa gag ctc agc agt att gac acg ctg gaa att aat gga						724
His Arg Phe Lys Glu Leu Ser Ser Ile Asp Thr Leu Glu Ile Asn Gly						
	140		145		150	
gac atc cac tta ctg gaa caa tca ttc aat caa aag agt gaa atg aag						772
Asp Ile His Leu Leu Glu Gln Ser Phe Asn Gln Lys Ser Glu Met Lys						
	155		160		165	
cac att aac aaa gca gga ggc gcc acg gac cgc ctc cct cca cac cgc						820
His Ile Asn Lys Ala Gly Gly Ala Thr Asp Arg Leu Pro Pro His Arg						
	170		175		180	185
tcc ttc cgc ctt cat tcc ttg ccc aca ggc ttg cac tgg aag ctg aat						868
Ser Phe Arg Leu His Ser Leu Pro Thr Gly Leu His Trp Lys Leu Asn						
	190		195		200	
aag aat ccc caa aac tca aac ttc cta ggg atg cca ccc ctt tag						913
Lys Asn Pro Gln Asn Ser Asn Phe Leu Gly Met Pro Pro Leu *						
	205		210		215	
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gcgtttattc	acttcattat	gttcattaag	ctttcatctt	agaataccag	tttcaccatt	1933
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 <212> PRT
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<400> 14

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			20					25					30		
Val	Ile	Cys	Gly	His	Val	Pro	Ser	Asp	Ala	Asp	Arg	Phe	Gln	Val	Asp
		35					40					45			
Leu	Gln	Asn	Gly	Ser	Ser	Val	Lys	Pro	Arg	Ala	Asp	Val	Ala	Phe	His
		50				55					60				
Phe	Asn	Pro	Arg	Phe	Lys	Arg	Ala	Gly	Cys	Ile	Val	Cys	Asn	Thr	Leu
65					70				75					80	
Ile	Asn	Glu	Lys	Trp	Gly	Arg	Glu	Glu	Ile	Thr	Tyr	Asp	Thr	Pro	Phe
			85					90					95		
Lys	Arg	Glu	Lys	Ser	Phe	Glu	Ile	Val	Ile	Met	Val	Leu	Lys	Asp	Lys
			100					105					110		
Phe	Gln	Val	Ala	Val	Asn	Gly	Lys	His	Thr	Leu	Leu	Tyr	Gly	His	Arg
		115					120					125			
Ile	Gly	Pro	Glu	Lys	Ile	Asp	Thr	Leu	Gly	Ile	Tyr	Gly	Lys	Val	Asn
	130					135					140				
Ile	His	Ser	Ile	Gly	Phe	Ser	Phe	Ser	Ser	Asp	Leu	Gln	Ser	Thr	Gln
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Ala	Ser	Ser	Leu	Glu	Leu	Thr	Glu	Ile	Ser	Arg	Glu	Asn	Val	Pro	Lys
			165					170					175		
Ser	Gly	Thr	Pro	Gln	Leu	Ser	Leu	Pro	Phe	Ala	Ala	Arg	Leu	Asn	Thr
			180					185					190		
Pro	Met	Gly	Pro	Gly	Arg	Thr	Val	Val	Lys	Gly	Glu	Val	Asn	Ala	
		195					200				205				
Asn	Ala	Lys	Ser	Phe	Asn	Val	Asp	Leu	Leu	Ala	Gly	Lys	Ser	Lys	Asp
	210					215					220				
Ile	Ala	Leu	His	Leu	Asn	Pro	Arg	Leu	Asn	Ile	Lys	Ala	Phe	Val	Arg
225					230					235				240	
Asn	Ser	Phe	Leu	Gln	Glu	Ser	Trp	Gly	Glu	Glu	Glu	Arg	Asn	Ile	Thr
			245					250					255		
Ser	Phe	Pro	Phe	Ser	Pro	Gly	Met	Tyr	Phe	Glu	Met	Ile	Ile	Tyr	Cys
		260						265					270		
Asp	Val	Arg	Glu	Phe	Lys	Val	Ala	Val	Asn	Gly	Val	His	Ser	Leu	Glu
		275					280					285			
Tyr	Lys	His	Arg	Phe	Lys	Glu	Leu	Ser	Ser	Ile	Asp	Thr	Leu	Glu	Ile
	290					295					300				
Asn	Gly	Asp	Ile	His	Leu	Leu	Glu	Val	Arg	Ser	Trp				
305					310						315				

<210> 15
 <211> 358
 <212> PRT
 <213> Homo sapiens

<400> 15

Met	Leu	Ser	Leu	Asn	Asn	Leu	Gln	Asn	Ile	Ile	Tyr	Asn	Pro	Val	Ile
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

1		5		10		15									
Pro	Tyr	Val	Gly	Thr	Ile	Pro	Asp	Gln	Leu	Asp	Pro	Gly	Thr	Leu	Ile
		20						25					30		
Val	Ile	Cys	Gly	His	Val	Pro	Ser	Asp	Ala	Asp	Arg	Phe	Gln	Val	Asp
		35					40					45			
Leu	Gln	Asn	Gly	Ser	Ser	Val	Lys	Pro	Arg	Ala	Asp	Val	Ala	Phe	His
		50					55				60				
Phe	Asn	Pro	Arg	Phe	Lys	Arg	Ala	Gly	Cys	Ile	Val	Cys	Asn	Thr	Leu
65					70				75					80	
Ile	Asn	Glu	Lys	Trp	Gly	Arg	Glu	Glu	Ile	Thr	Tyr	Asp	Thr	Pro	Phe
			85						90					95	
Lys	Arg	Glu	Lys	Ser	Phe	Glu	Ile	Val	Ile	Met	Val	Leu	Lys	Asp	Lys
			100					105					110		
Phe	Gln	Val	Ala	Val	Asn	Gly	Lys	His	Thr	Leu	Leu	Tyr	Gly	His	Arg
		115					120					125			
Ile	Gly	Pro	Glu	Lys	Ile	Asp	Thr	Leu	Gly	Ile	Tyr	Gly	Lys	Val	Asn
		130				135					140				
Ile	His	Ser	Ile	Gly	Phe	Ser	Phe	Ser	Ser	Asp	Leu	Gln	Ser	Thr	Gln
145					150				155					160	
Ala	Ser	Ser	Leu	Glu	Leu	Thr	Glu	Ile	Ser	Arg	Glu	Asn	Val	Pro	Lys
			165						170					175	
Ser	Gly	Thr	Pro	Gln	Leu	Pro	Ser	Asn	Arg	Gly	Gly	Asp	Ile	Ser	Lys
			180					185					190		
Ile	Ala	Pro	Arg	Thr	Val	Tyr	Thr	Lys	Ser	Lys	Asp	Ser	Thr	Val	Asn
		195					200					205			
His	Thr	Leu	Thr	Cys	Thr	Lys	Ile	Pro	Pro	Met	Asn	Tyr	Val	Ser	Lys
		210				215					220				
Ser	Leu	Pro	Phe	Ala	Ala	Arg	Leu	Asn	Thr	Pro	Met	Gly	Pro	Gly	Arg
225					230				235					240	
Thr	Val	Val	Val	Lys	Gly	Glu	Val	Asn	Ala	Asn	Ala	Lys	Ser	Phe	Asn
			245						250					255	
Val	Asp	Leu	Leu	Ala	Gly	Lys	Ser	Lys	Asp	Ile	Ala	Leu	His	Leu	Asn
			260					265					270		
Pro	Arg	Leu	Asn	Ile	Lys	Ala	Phe	Val	Arg	Asn	Ser	Phe	Leu	Gln	Glu
		275					280					285			
Ser	Trp	Gly	Glu	Glu	Glu	Arg	Asn	Ile	Thr	Ser	Phe	Pro	Phe	Ser	Pro
		290				295					300				
Gly	Met	Tyr	Phe	Glu	Met	Ile	Ile	Tyr	Cys	Asp	Val	Arg	Glu	Phe	Lys
305					310				315					320	
Val	Ala	Val	Asn	Gly	Val	His	Ser	Leu	Glu	Tyr	Lys	His	Arg	Phe	Lys
			325						330					335	
Glu	Leu	Ser	Ser	Ile	Asp	Thr	Leu	Glu	Ile	Asn	Gly	Asp	Ile	His	Leu
			340					345					350		
Leu	Glu	Val	Arg	Ser	Trp										
		355													

<210> 16
 <211> 368
 <212> PRT
 <213> Homo sapiens

<400> 16
Met Leu Ser Leu Asn Asn Leu Gln Asn Ile Ile Tyr Asn Pro Val Ile
1 5 10 15
Pro Tyr Val Gly Thr Ile Pro Asp Gln Leu Asp Pro Gly Thr Leu Ile
20 25 30
Val Ile Cys Gly His Val Pro Ser Asp Ala Asp Arg Phe Gln Val Asp
35 40 45
Leu Gln Asn Gly Ser Ser Val Lys Pro Arg Ala Asp Val Ala Phe His
50 55 60
Phe Asn Pro Arg Phe Lys Arg Ala Gly Cys Ile Val Cys Asn Thr Leu
65 70 75 80

Ile	Asn	Glu	Lys	Trp	Gly	Arg	Glu	Glu	Ile	Thr	Tyr	Asp	Thr	Pro	Phe	85	90	95
Lys	Arg	Glu	Lys	Ser	Phe	Glu	Ile	Val	Ile	Met	Val	Leu	Lys	Asp	Lys	100	105	110
Phe	Gln	Val	Ala	Val	Asn	Gly	Lys	His	Thr	Leu	Leu	Tyr	Gly	His	Arg	115	120	125
Ile	Gly	Pro	Glu	Lys	Ile	Asp	Thr	Leu	Gly	Ile	Tyr	Gly	Lys	Val	Asn	130	135	140
Ile	His	Ser	Ile	Gly	Phe	Ser	Phe	Ser	Ser	Asp	Leu	Gln	Ser	Thr	Gln	145	150	155
Ala	Ser	Ser	Leu	Glu	Leu	Thr	Glu	Ile	Ser	Arg	Glu	Asn	Val	Pro	Lys	165	170	175
Ser	Gly	Thr	Pro	Gln	Leu	Ser	Leu	Pro	Phe	Ala	Ala	Arg	Leu	Asn	Thr	180	185	190
Pro	Met	Gly	Pro	Gly	Arg	Thr	Val	Val	Val	Lys	Gly	Glu	Val	Asn	Ala	195	200	205
Asn	Ala	Lys	Ser	Phe	Asn	Val	Asp	Leu	Leu	Ala	Gly	Lys	Ser	Lys	Asp	210	215	220
Ile	Ala	Leu	His	Leu	Asn	Pro	Arg	Leu	Asn	Ile	Lys	Ala	Phe	Val	Arg	225	230	235
Asn	Ser	Phe	Leu	Gln	Glu	Ser	Trp	Gly	Glu	Glu	Glu	Arg	Asn	Ile	Thr	245	250	255
Ser	Phe	Pro	Phe	Ser	Pro	Gly	Met	Tyr	Phe	Glu	Met	Ile	Ile	Tyr	Cys	260	265	270
Asp	Val	Arg	Glu	Phe	Lys	Val	Ala	Val	Asn	Gly	Val	His	Ser	Leu	Glu	275	280	285
Tyr	Lys	His	Arg	Phe	Lys	Glu	Leu	Ser	Ser	Ile	Asp	Thr	Leu	Glu	Ile	290	295	300
Asn	Gly	Asp	Ile	His	Leu	Glu	Gln	Ser	Phe	Asn	Gln	Lys	Ser	Glu		305	310	315
Met	Lys	His	Ile	Asn	Lys	Ala	Gly	Gly	Ala	Thr	Asp	Arg	Leu	Pro	Pro	325	330	335
His	Arg	Ser	Phe	Arg	Leu	His	Ser	Leu	Pro	Thr	Gly	Leu	His	Trp	Lys	340	345	350
Leu	Asn	Lys	Asn	Pro	Gln	Asn	Ser	Asn	Phe	Leu	Gly	Met	Pro	Pro	Leu	355	360	365

<210> 17

<211> 215

<212> PRT

<213> Homo sapiens

<400> 17

Met	Leu	Ser	Leu	Asn	Asn	Leu	Gln	Asn	Ile	Ile	Tyr	Asn	Pro	Val	Ile	1	5	10	15
Pro	Tyr	Val	Gly	Thr	Ile	Pro	Asp	Gln	Leu	Asp	Pro	Gly	Thr	Leu	Ile	20	25	30	
Val	Ile	Cys	Gly	His	Val	Pro	Ser	Asp	Ala	Asp	Arg	Phe	Gln	Val	Asp	35	40	45	
Leu	Gln	Asn	Gly	Ser	Ser	Val	Lys	Pro	Arg	Ala	Asp	Val	Ala	Phe	His	50	55	60	
Phe	Asn	Pro	Arg	Phe	Lys	Arg	Ala	Gly	Cys	Ile	Val	Cys	Asn	Thr	Leu	65	70	75	80
Ile	Asn	Glu	Lys	Trp	Gly	Arg	Glu	Glu	Ile	Thr	Tyr	Asp	Thr	Pro	Phe	85	90	95	
Lys	Arg	Glu	Lys	Ser	Phe	Glu	Ile	Val	Ile	Met	Val	Leu	Lys	Asp	Lys	100	105	110	
Phe	Gln	Met	Ile	Ile	Tyr	Cys	Asp	Val	Arg	Glu	Phe	Lys	Val	Ala	Val	115	120	125	
Asn	Gly	Val	His	Ser	Leu	Glu	Tyr	Lys	His	Arg	Phe	Lys	Glu	Leu	Ser	130	135	140	
Ser	Ile	Asp	Thr	Leu	Glu	Ile	Asn	Gly	Asp	Ile	His	Leu	Leu	Glu	Gln				

145		150		155		160									
Ser	Phe	Asn	Gln	Lys	Ser	Glu	Met	Lys	His	Ile	Asn	Lys	Ala	Gly	Gly
		165		170		175									
Ala	Thr	Asp	Arg	Leu	Pro	Pro	His	Arg	Ser	Phe	Arg	Leu	His	Ser	Leu
		180		185		190									
Pro	Thr	Gly	Leu	His	Trp	Lys	Leu	Asn	Lys	Asn	Pro	Gln	Asn	Ser	Asn
		195		200		205									
Phe	Leu	Gly	Met	Pro	Pro	Leu									
	210				215										

<210> 18
 <211> 504
 <212> DNA
 <213> Homo sapiens

<220>
 <221> allele
 <222> 81
 <223> 99-7177-81 : polymorphic base C or T

<220>
 <221> misc_binding
 <222> 69..93
 <223> 99-7177-81.probe

<220>
 <221> primer_bind
 <222> 62..80
 <223> 99-7177-81.mis

<220>
 <221> primer_bind
 <222> 82..100
 <223> 99-7177-81.mis complement

<220>
 <221> primer_bind
 <222> 1..20
 <223> 99-7177.pu

<220>
 <221> primer_bind
 <222> 484..504
 <223> 99-7177.rp complement

<400> 18
 aatcctgacc caccttctcc caagcacgca tgtagaggaa agaaagcaag agcgatagct 60
 gaggggatca gcctactaga yggaggcagg tgtttcaaga tgggtgttga agggcaagcc 120
 gagaactcta gtagcgggga ggggaaaact aaaactttat tactgtaagc aaatatcaca 180
 gcaaatacagc cttaagtagg tataaaaagaa cccataaaaag aagacaaaat gtaaccaaag 240
 ctcaccagac cacagaagag tcatcactgg agtcggaaga cagacgcgct ggatcctgca 300
 gtaggagttg gggcatcccc cagcatagga caacagcaac cttcaatcct ccttcgtata 360
 agtcctttt attaagtcca attgttactt tgggcaccct ctggtgtttg ctggtgaggg 420
 ccttcccca gcaagcaaca ctgaaacagt ggttctggga gcagcgtcct gggacgcgtt 480
 ccaggacttg agttaatttc tggg 504

<210> 19
 <211> 488
 <212> DNA
 <213> Homo sapiens

<220>

<221> allele
 <222> 345
 <223> 99-7212-345 : polymorphic base C or T

<220>
 <221> misc_binding
 <222> 333..357
 <223> 99-7212-345.probe

<220>
 <221> primer_bind
 <222> 326..344
 <223> 99-7212-345.mis

<220>
 <221> primer_bind
 <222> 346..364
 <223> 99-7212-345.mis complement

<220>
 <221> primer_bind
 <222> 1..20
 <223> 99-7212.pu

<220>
 <221> primer_bind
 <222> 470..488
 <223> 99-7212.rp complement

<400> 19
 gctccttatg taattgaatg aatggatatt ttatcagatg ctttttaaaa gtcagtacac 60
 aattccatct atttcacagc aaattctaca gaaatagcag ctagacagca ggaagctgtg 120
 gcttactgtt tagtgacttg tgattgtaat taaatgatta gtcttcact ccattccctc 180
 caactgtct tgggtctggg gaggtaggga ggacaaatgc aaaatccata gagtcaagga 240
 tatagtgagg agtttacttt gccattgact ctgacaatca atcgtcagtg agacatgctg 300
 attgtgatga gaacatgact aaagacaaga ttcttcaag gtagygtct cactgtttca 360
 ttcaatgaaa aactattggg gttgtataac ccaatgaatc atttttgtat tttgaatctt 420
 taaaaatata tacaagtgtt attttgcttg aagtgtgtt tatttataag gttgacaatt 480
 aaactgac 488

<210> 20
 <211> 542
 <212> DNA
 <213> Homo sapiens

<220>
 <221> allele
 <222> 226
 <223> 99-7193-228 : polymorphic base G or C

<220>
 <221> misc_binding
 <222> 214..238
 <223> 99-7193-228.probe

<220>
 <221> primer_bind
 <222> 207..225
 <223> 99-7193-228.mis

<220>
 <221> primer_bind

<222> 227..245
<223> 99-7193-228.mis complement

<220>
<221> primer_bind
<222> 1..20
<223> 99-7193.pu

<220>
<221> primer_bind
<222> 522..542
<223> 99-7193.rp complement

<400> 20
gaggtaaaaa tagcaggcag gagaacagat ctttttaggat tgtgaattgt aatgtggaac 60
atgaaaactt catcatcttc tgtgtgctgg ctagtgtcag ttatcctttg ctgtataaaa 120
atcaccccca aaatttagtga tttgaaacaa ctgtcccat ttatttactc atgattttgc 180
agttgtcag gacttggtgg ggataccttg actctgcttc tcgcastgtt gactgaqgtc 240
atacttgtag ctacattcag ctggcagctt cattggggct ggaacagcaa agacagcttc 300
cctaacatac ctggcacctc agccaagggtg gctgcaatgg ctggaggctc actgggcctt 360
tcacttctgt gtggtttctc gtgatttcgt agtctatcct gaactccttt tcacggcaac 420
tggaatgcaa aaagatgaaa acagaagcta caatgtctgg gaacagaagt cctagaatgt 480
cacttctact acacctatta ctactatta gtcaaaataa actcctctcc caatacttct 540
ca 542

<210> 21
<211> 528
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 212
<223> 99-7186-212 : polymorphic base A or G

<220>
<221> misc_binding
<222> 200..224
<223> 99-7186-212.probe

<220>
<221> primer_bind
<222> 193..211
<223> 99-7186-212.mis

<220>
<221> primer_bind
<222> 213..231
<223> 99-7186-212.mis complement

<220>
<221> primer_bind
<222> 1..19
<223> 99-7186.pu

<220>
<221> primer_bind
<222> 510..528
<223> 99-7186.rp complement

<400> 21
gagtgccatg tgtgcataga ttgttgtctg gggtttttcc tttttgttac ttctgcaata 60

tttagaacag	tgactgacac	atatcaggca	ctcaataatt	atttgctgaa	tttctcaatg	120
tctcgatttg	gcataaggat	ttcattttcc	catgggtatat	tttcttccgt	ggattgatgg	180
gctagtagta	atttgacacg	gtgtcttggg	grttcacaa	catgggttta	atgtcccagt	240
cccccttggc	tacaggaggt	acttgatcct	aggtgactaa	ggcagaaata	aatagaatgt	300
gtaggaactcc	tctgggtgta	aaagtcacgg	gttccaaaag	ttcattttata	agtcaattgt	360
ttggacatcc	tgaacttatt	ttcagaacac	gattgggcac	agctagttaa	ctgcaggagg	420
gcctgaggag	actggaagg	gccagaacct	ggaaccagat	ctgcccacta	ggacaggacc	480
agccctggaa	ggacaggagc	aggtgcactg	gattctaaag	gtgttcag		528

<210> 22

<211> 531

<212> DNA

<213> Homo sapiens

<220>

<221> allele

<222> 49

<223> 99-7182-49 : polymorphic base C or T

<220>

<221> misc_binding

<222> 37..61

<223> 99-7182-49.probe

<220>

<221> primer_bind

<222> 30..48

<223> 99-7182-49.mis

<220>

<221> primer_bind

<222> 50..68

<223> 99-7182-49.mis complement

<220>

<221> primer_bind

<222> 1..20

<223> 99-7182.pu

<220>

<221> primer_bind

<222> 511..531

<223> 99-7182.rp complement

<400> 22

gtgtgtagaa	aagaaagatg	gctgtcattt	gagttgttaa	gaacagcayg	ctgcaatacc	60
aaaacatcaa	gctgtacatc	tcaaatatgt	atgattttca	tatgtgaatc	acatctcaat	120
aaagctgtta	gaaaaataaa	attaccatta	agtttaaaaa	aaaaaagaaa	aaaagaaaaa	180
aacaaccaca	gtcggggcaa	gggccatggt	actagggcca	gggatttggc	caatgaagca	240
ggaacataga	gacccatagg	ccataaggaa	aagaagattc	aaggaaggcc	aggacatggg	300
agggaatgaa	caaactccag	tcctagaggt	ttagcagaga	ctagctggct	tcttgcaagt	360
aattaataaa	tgagaaaaaa	atctgagatc	acaataaaaag	atctttactg	gtgcaagggc	420
cactttctac	cgtgttttga	ctgcttttgg	tcattcttta	gtaccttaag	ttttttatat	480
tttgtgaaga	ttttactatt	ttttwatctg	caagagagta	agttcaatca	a	531

<210> 23

<211> 546

<212> DNA

<213> Homo sapiens

<220>

<221> allele

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<222> 372
<223> 99-1585-373 : polymorphic base C or T

<220>
<221> misc_binding
<222> 360..384
<223> 99-1585-373.probe

<220>
<221> primer_bind
<222> 353..371
<223> 99-1585-373.mis

<220>
<221> primer_bind
<222> 373..391
<223> 99-1585-373.mis complement

<220>
<221> primer_bind
<222> 1..20
<223> 99-1585.pu

<220>
<221> primer_bind
<222> 527..546
<223> 99-1585.rp complement

<220>
<221> misc_feature
<222> 52..53,55
<223> n=a, g, c or t

<400> 23
cctgcaacat ttttwtatgtg tagaattctg tgaatgaatc caacttcggc anntnttttt 60
ttctttttctt ttttttaatc aaggaagtgg agacaagatg tgaaggggtg gcctgcccct 120
ccacacctgt ggatatttct agtcagggtg gacgagagac tgagaaaata aataaaacac 180
agagacaaag tatagagaaa caacagtggg cccagggaac cggcgctcag cataccaagg 240
acctgcaccg gcaccatctc tgagtccct cagtttttat tgattattat cttcgttatt 300
tcagcaaaaa ggaatgtagt aggagagcag ggtgataata aggagaaggt cagcaacgaa 360
catgtgagca ayagaatcta cgtcataatk aagttcaagg gaaggtacta tgactggacg 420
tgcahgtaag ccagatttat gtttctctcc acccaaacat ctcggtggag taaagaataa 480
caaggcagca ttgctgcaaa catgtctcgc ctcccgccat agggcggttt ttctcctatc 540
tcagaa 546

<210> 24
<211> 396
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 278
<223> 99-1587-281 : polymorphic base A or G

<220>
<221> misc_binding
<222> 266..290
<223> 99-1587-281.probe

<220>
<221> primer_bind

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<222> 259..277
<223> 99-1587-281.mis

<220>
<221> primer_bind
<222> 279..297
<223> 99-1587-281.mis complement

<220>
<221> primer_bind
<222> 1..21
<223> 99-1587.pu

<220>
<221> primer_bind
<222> 377..396
<223> 99-1587.rp complement

<220>
<221> misc_feature
<222> 48
<223> n=a, g, c or t

<400> 24
taatggtagt tgatgaggtc ctatgtaata tgcatttctt tggttgcnaa tagcaaatta 60
ctacacacac agaaaggaaa gccacactcc ccgacacdwc tacacacagg aggactcaca 120
caggagggag actcaaagaa ggcacgtgac ttttacattg ttagggctta catggtcctg 180
ggatttccca ccagtactca aaagatcaat tgtatgaaca agtcacctat ttttacggca 240
ctaaataatt attattcaac aacatggaaa atatgtgrta gcagacctgg attttcctta 300
agagttattt ttatgtggtg ctgccccctg ctggaatata acatctatac acatcctttc 360
tggtctgggt gacatcctaa aaccagccca ggacca 396

<210> 25
<211> 447
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 283
<223> 99-13798-284 : polymorphic base A or G

<220>
<221> misc_binding
<222> 271..295
<223> 99-13798-284.probe

<220>
<221> primer_bind
<222> 264..282
<223> 99-13798-284.mis

<220>
<221> primer_bind
<222> 284..302
<223> 99-13798-284.mis complement

<220>
<221> primer_bind
<222> 1..20
<223> 99-13798.pu

<220>
 <221> primer_bind
 <222> 427..447
 <223> 99-13798.rp complement

<220>
 <221> misc_feature
 <222> 34,416
 <223> n=a, g, c or t

<400> 25
 gaggaaaagg actttggatg tctgggtgtca ctgnctgcac accaggcaca cagcaggtgc 60
 tcaataagta tttgatgaat atatcaaagt aatgaggagt gtgacacagt tcaagaagaa 120
 aatcaaataga aaaattaggc ttcttagcag cccgaaaaga gctctttatc tagaaattgt 180
 caaacacagct gatgcaagtt tttttgggtg taacaaggca gccgcaagat tgctatggag 240
 aggacaccgt gtaccatgga gattaacggc atgagcttta gcrgcagcta accccgtgca 300
 gatgtgtgac ttggacaggt tactgagctt gctaagcccc tgtctcactc tccaaacagg 360
 gataatgaca cctctctcac aagggtggtg tgaggattaa atgaggtaat cttttnaagc 420
 tcccatccta gcacacgtaa gaagcat 447

<210> 26
 <211> 506
 <212> DNA
 <213> Homo sapiens

<220>
 <221> allele
 <222> 402
 <223> 99-1601-402 : polymorphic base A or T

<220>
 <221> misc_binding
 <222> 390..414
 <223> 99-1601-402.probe

<220>
 <221> primer_bind
 <222> 383..401
 <223> 99-1601-402.mis

<220>
 <221> primer_bind
 <222> 403..421
 <223> 99-1601-402.mis complement

<220>
 <221> primer_bind
 <222> 1..18
 <223> 99-1601.pu

<220>
 <221> primer_bind
 <222> 486..506
 <223> 99-1601.rp complement

<400> 26
 ttggcttggc agggcaacca gctcaccaga ctctctgcag acccgaagtc attacatata 60
 gtatgataac agggaatgga cccgaccagc atttgctgga gatgatattc ggtgtcagcc 120
 cgacaggccc ctacctgctt ctcttgatat gcagggaatcc cttcaagctc caacaagatc 180
 tgtttaatag actggagagt ccttttagttc ctctctctaa gggaaaatca gatcgttctg 240
 gtttgcttgg taactcctta cttcatccct gatgggaagt ttatagaatg aggaaccagg 300
 gctattacat gaaactataa aactgcctag agcacatact tggtattttt aacattgttg 360

agaggggactc acttaattca gccttgccagc tattgcattc cwgtccaaac caacggcagg	420
ttctcaaaac aagcggtgaa agggttcctg ttgcagagct gtctggacat ttaaagaagg	480
gagaggaaat ctccarggggt cgggttg	506

<210> 27
 <211> 546
 <212> DNA
 <213> Homo sapiens

<220>
 <221> allele
 <222> 79
 <223> 99-13808-80 : polymorphic base A or T

<220>
 <221> misc_binding
 <222> 67..91
 <223> 99-13808-80.probe

<220>
 <221> primer_bind
 <222> 60..78
 <223> 99-13808-80.mis

<220>
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 <222> 80..98
 <223> 99-13808-80.mis complement

<220>
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 <222> 1..20
 <223> 99-13808.pu

<220>
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 <222> 526..546
 <223> 99-13808.rp complement

<220>
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 <222> 266
 <223> 99-13808-268 : polymorphic base A or C

<220>
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 <222> 254..278
 <223> 99-13808-268.probe

<220>
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 <222> 247..265
 <223> 99-13808-268.mis

<220>
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 <222> 267..285
 <223> 99-13808-268.mis complement

<220>
 <221> allele
 <222> 419

<223> 99-13808-425 : polymorphic base G or C

<220>

<221> misc_binding

<222> 407..431

<223> 99-13808-425.probe

<220>

<221> primer_bind

<222> 400..418

<223> 99-13808-425.mis

<220>

<221> primer_bind

<222> 420..438

<223> 99-13808-425.mis complement

<220>

<221> allele

<222> 453

<223> 99-13808-455 : polymorphic base A or G

<220>

<221> misc_binding

<222> 441..465

<223> 99-13808-455.probe

<220>

<221> primer_bind

<222> 434..452

<223> 99-13808-455.mis

<220>

<221> primer_bind

<222> 454..472

<223> 99-13808-455.mis complement

<400> 27

gttgtgcctt	aaagaatttg	ctcatccaca	gagtgccaac	tgcattagaa	agaaaacaac	60
tctcctttct	aactcaccwg	cattgatttt	ctgttggttg	catgtagaag	agtatttcaa	120
agaatgaatg	aaagctataa	tatttattag	aagtaaaaaa	gttctaaaga	tatgctacct	180
tactgggatg	cttagagacc	atttgcaaac	cctgtttatg	atctagaaat	cctgtttttc	240
atttttttatt	tgtaaaactc	tataamtctc	aaaaaatttt	aggtggatta	tcatgtacct	300
aagggtaaaa	tatagttgaa	attattctta	cctgattttt	catatctgaa	tttcgtgggc	360
agttcaaagt	aattgtatca	cattcttcag	ctaggaaaaa	aaaaaagaaa	gaaagaaasa	420
aacaaagtgt	gatttttaaa	agcacacact	cctggtgtga	agacctaaaa	ttaaggttca	480
gtgtcacatg	ctgccttggc	atctggtaaa	atcagaagag	ctggactaca	aatycctctc	540
caaact						546

<210> 28

<211> 476

<212> DNA

<213> Homo sapiens

<220>

<221> allele

<222> 212

<223> 99-13810-214 : polymorphic base C or T

<220>

<221> misc_binding

<222> 200..224

<223> 99-13810-214.probe

<220>

<221> primer_bind

<222> 193..211

<223> 99-13810-214.mis

<220>

<221> primer_bind

<222> 213..231

<223> 99-13810-214.mis complement

<220>

<221> primer_bind

<222> 1..18

<223> 99-13810.pu

<220>

<221> primer_bind

<222> 458..476

<223> 99-13810.rp complement

<220>

<221> allele

<222> 168

<223> 99-13810-170 : polymorphic base A or T

<220>

<221> misc_binding

<222> 156..180

<223> 99-13810-170.probe

<220>

<221> primer_bind

<222> 149..167

<223> 99-13810-170.mis

<220>

<221> primer_bind

<222> 169..187

<223> 99-13810-170.mis complement

<400> 28

gcattccag	attgtaacat	agttttaagt	aaacatccac	tgaaagtctg	catggaagaa	60
cacagaagcc	agagcaagtt	cagggctcct	agaaagacga	tgctggagct	agccctagag	120
aatggctgag	aattggatga	actcagaaga	agcagcaaag	tagttgcwgg	tggcaggcat	180
ggcaggagaa	gggatcaggt	ggctggaaga	gyggagggta	tagaactgaa	acagagagtc	240
tgttggaggt	ggacagagga	aggcgggatt	agatgagaaa	tgacggaccc	agtttctaag	300
aaagaccaag	aaagataagc	aaagggatgt	aggtgggatg	cccttctagg	ttctcgggaa	360
acttgctacc	tgctttgcac	tgactttgca	tgagggaaga	tggtcaacac	agtcttgcaa	420
gaagtcagac	aagcaggcaa	tgacaattct	ctgagatggc	aaatagggat	tgggct	476

<210> 29

<211> 454

<212> DNA

<213> Homo sapiens

<220>

<221> allele

<222> 127

<223> 99-13790-129 : polymorphic base C or T

<220>
 <221> misc_binding
 <222> 115..139
 <223> 99-13790-129.probe

<220>
 <221> primer_bind
 <222> 108..126
 <223> 99-13790-129.mis

<220>
 <221> primer_bind
 <222> 128..146
 <223> 99-13790-129.mis complement

<220>
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 <222> 1..20
 <223> 99-13790.pu

<220>
 <221> primer_bind
 <222> 434..454
 <223> 99-13790.rp complement

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 gtcatttttac taagcctttc agacagtaga gagtgggatt atacttgtcc caacagctca 60
 cctctctaaa ggtcaaacct aaaccatttt ggttctcttg ttcaagttca ggttgccagt 120
 gaaaagyaaa ggaacttgaa attcatgtta aacatttaac atctttccat atgaattgct 180
 aggaagcaac ttccattcca aagttgtgtt aacttcacag tttcccacc tgtggtgaag 240
 atggtacaaa atagcttaaa aactgatttt gttccatcag attctaattct ttagtcacag 300
 aattcaaggc catactctaa actttaaggt tggcagaaat atattataac agaaatttta 360
 gcaccatgta aatgttttaa gttatttagc cttaaataca gaaccattta actcagggtt 420
 gaaaagtcag gatgaagtga gggwttgatt gatt 454

<210> 30
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 <212> DNA
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<220>
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 <222> 153
 <223> 99-13809-153 : polymorphic base A or G

<220>
 <221> misc_binding
 <222> 141..165
 <223> 99-13809-153.probe

<220>
 <221> primer_bind
 <222> 134..152
 <223> 99-13809-153.mis

<220>
 <221> primer_bind
 <222> 154..172
 <223> 99-13809-153.mis complement

<220>
 <221> primer_bind

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<222> 1..21
<223> 99-13809.pu

<220>
<221> primer_bind
<222> 424..444
<223> 99-13809.rp complement

<400> 30
caactgagtg aagagcaatg ggaatttgta gactttacag atgacatcac ccccatcata      60
cacgatgaag ctcagcagac agttgctgct ttccatccct taaccaggat atccctgata      120
aaggaaggac ccaagattag caaaactggc caracttcag gcagtcatct tattgctgga      180
tgtcctggcc aacaaatcgc cccatctgca cagtttttat aaatttttgg accattgcct      240
aagagttgca ccctttgtgg taaagaactc tcagaatctc ttgcctcaaa tacacccaaa      300
ctataaataa agaaacagat gtctctatgt acagcaaggc caccatacaa ggcttcagca      360
gaacatttcc agtctccttt ggagtcccac ttattactga cagtgagcaa gacactcatt      420
tctcttctaa gaacatacaa cgcc                                         444

<210> 31
<211> 693
<212> DNA
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<220>
<221> allele
<222> 162
<223> 99-1597-162 : polymorphic base A or G

<220>
<221> misc_binding
<222> 150..174
<223> 99-1597-162.probe

<220>
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<222> 143..161
<223> 99-1597-162.mis

<220>
<221> primer_bind
<222> 163..181
<223> 99-1597-162.mis complement

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<222> 1..19
<223> 99-1597.pu

<220>
<221> primer_bind
<222> 675..693
<223> 99-1597.rp complement

<220>
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<222> 582..615
<223> n=a, g, c or t

<400> 31
tttaagatgc caagttgtca aactgggcag ctaggcccca ggctctttct aaattgtcaa      60
gactagcaaaa gccgagtcac cccctgctc tagttctgga tgacaccaag cctaggaaat      120
aaagcacaat agatggggcc ctggctctctg aatgacagag trtgcatggg ggctaggagg      180

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aaggaggaat	ccagctctct	aaaaggaagg	tgcaggcggt	gtgtgagggg	tcaaagacaa	240
aggggcgtgt	cccactgaag	atacaaactc	taggccgggc	gcggtggctc	atgcctgtaa	300
tcccagtact	ttgggatgcc	aaggcgggca	gatcacaagg	tcaggagatc	gagaccatct	360
tggctaaggg	ggtgaaaccc	tgtctctact	aaaaaaacta	caaaaagtta	gccaggtgtg	420
gtagcatacg	cctgtagtcc	cagctactca	ggaggctgag	gcaggagaa	tgcttgaacc	480
cgggagatgg	aggttgcagt	gagccaagat	cacgccactg	cactccagcc	tgggcaacag	540
agcgagactc	tgtctcaaaa	aggaaaagaa	aaagaaaaag	annnnnnnnn	nnnnnnnnnn	600
nnnnnnnnnn	nnnnnaatag	atttctgttt	ccttgatgag	gaaacaagat	aaaactagtc	660
actatgtatt	gggtggctac	tttagcatca	atc			693

<210> 32
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ggcgatgac	tctctttgga aaccac
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tgctaaagac	gagagactcc tcgcc
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<210> 34
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<220>
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ccccctatga	tctgattcac caggcttac
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<210> 35
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 <210> 41
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 <212> DNA
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 <210> 42
 <211> 25
 <212> DNA
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<220>
 <223> oligonucleotide PCTAexBLR140

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 <210> 43
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 <210> 44
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 gggaatggtg ccaacatacg ggattac 27

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 <210> 46
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 <220>
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 <400> 46
 tcacctacac ctcacccact tcctc 25

 <210> 47
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<210> 48
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 <220>
 <223> oligonucleotide PCTAex9terLR330

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<223> oligonucleotide PCTAexCLF120	
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 tgtaaaacga cggccagt 18
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 <223> sequencing oligonucleotide PrimerRP
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 caggaaacag ctatgacc 18